

DERWENT-ACC-NO: 2000-350149  
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TITLE: Sequencing nucleotide sequences e.g. for genome mapping  
uses probes  
comprising a pattern of universal nucleotides, which pair with  
any natural  
nucleotide, and the designate nucleotides A, C, G or T

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PATENT-ASSIGNEE: UNIV BROWN RES FOUND[UYBRN]

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(October 13,  
1998)

PATENT-FAMILY:

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AU 200012046 A	May 1, 2000	N/A	000
C12Q 001/68			
WO 200022171	April 20, 2000	E	071
C12Q 001/68			
A2			

DESIGNATED-STATES: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CU  
CZ DE DK EE ES F  
I GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS  
LT LU LV MA MD  
MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ  
UA UG UZ VN YU  
ZA ZW AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU  
MC MW NL OA PT S  
D SE SL SZ TZ UG ZW

APPLICATION-DATA:

PUB-NO	APPL-DESCRIPTOR	APPL-NO
APPL-DATE		
AU 200012046A	N/A	2000AU-0012046
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October 13, 1999		
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INT-CL\_(IPC): B01J019/00; C12Q001/68 ; G06F019/00

ABSTRACTED-PUB-NO: WO 200022171A

BASIC-ABSTRACT: NOVELTY - A method for sequencing a nucleic acid is new and comprises providing a set of probes containing multiple copies of a pattern of universal and designate nucleotides, determining a spectrum of these probes which hybridize to a test sequence and ordering this spectrum to determine a sequence of a portion of the test sequence.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for:

(1) a nucleic acid probe (I) comprising sequence of universal and designate nucleotides orders in an iterative pattern

(2) a sequencing chip comprising a substrate and a set of (I);

(3) ordering a set of (I) into sequential order using a probe detector generating a spectrum signal representative of hybridized probes and a sequencer processing the signal as a function of a predetermined pattern of designate and universal nucleotides;

(4) ordering a spectrum of probes to determine a sequence of a portion of a test sequence, by: (i) providing a set of (I) which hybridize to a test sequence and in which the pattern requires a designate nucleotide at the 'mth' position and at the 'nth' position; (ii) identifying a subset of probes whose first m-1 nucleotides correspond to the last m-1 nucleotides of a growing sequence; and (iii) appending the nucleotide at the mth position to the growing sequence if a single nucleotide occurs at the mth position of all probes in the subset; and

(5) a computer-readable medium storing instructions directing a computer to store a spectrum signal representative of hybridized probes as in (5) and to perform the method of (5).

USE - The method is useful for full or partial sequencing of nucleic acid sequences, useful e.g. for genome sequencing, understanding the function and control of genes, gene mapping and genetic fingerprinting.

ADVANTAGE - The inclusion of universal nucleotides in the probes allows efficient and rapid sequencing by existing sequencing by hybridization techniques of longer nucleotide sequences than can be sequenced using traditional probes.

CHOSEN-DRAWING: Dwg.0/10

TITLE-TERMS:

SEQUENCE NUCLEOTIDE SEQUENCE GENOME MAP PROBE COMPRISE PATTERN  
UNIVERSAL PAIR  
NATURAL NUCLEOTIDE DESIGNATED

DERWENT-CLASS: B04 D16 T01

CPI-CODES: B04-E02; B04-E05; B11-C08E5; B12-K04E; B12-K04F;  
D05-H09; D05-H10;  
D05-H12; D05-H12D1; D05-H18A;

EPI-CODES: T01-E01A; T01-S03;

CHEMICAL-CODES:

Chemical Indexing M1 \*01\*

Fragmentation Code

M423 M424 M740 M750 M905 N102 N135 Q233

Specific Compounds

A00NSK A00NSA

Chemical Indexing M1 \*02\*

Fragmentation Code

M423 M424 M740 M750 M905 N102 N135 Q233

Specific Compounds

A012PK A012PA

Chemical Indexing M1 \*03\*

Fragmentation Code

M423 M424 M710 M740 M781 M905 N102 N135 P831 Q233

Q505

Specific Compounds

A00NSD A00NSN

Chemical Indexing M1 \*04\*

Fragmentation Code

M423 M424 M710 M740 M781 M905 N102 N135 P831 Q233  
Q505  
Specific Compounds  
A012PD A012PN

Chemical Indexing M6 \*05\*  
Fragmentation Code  
M905 P831 Q233 Q505 R502 R511 R515 R521 R627 R639

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